

Sungho Won

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

123
papers

5,850
citations

18
h-index

76
g-index

135
ext. papers

6,649
ext. citations

5
avg. IF

5.29
L-index

#	Paper	IF	Citations
123	Impact of statins on the survival of patients with cancer: a nationwide population-based cohort study in South Korea.. <i>Cancer Communications</i> , 2022 ,	9.4	
122	Unveiling genetic variants for age-related sarcopenia by conducting a genome-wide association study on Korean cohorts.. <i>Scientific Reports</i> , 2022 , 12, 3501	4.9	1
121	rs2671655 single nucleotide polymorphism modulates the risk for gastric cancer in Helicobacter pylori-infected individuals: a genome-wide association study in the Korean population.. <i>Gastric Cancer</i> , 2022 , 25, 573	7.6	
120	missForest with feature selection using binary particle swarm optimization improves the imputation accuracy of continuous data.. <i>Genes and Genomics</i> , 2022 , 1	2.1	1
119	Association between prenatal cadmium exposure and cord blood DNA methylation.. <i>Environmental Research</i> , 2022 , 113268	7.9	0
118	Disordered development of gut microbiome interferes with the establishment of the gut ecosystem during early childhood with atopic dermatitis.. <i>Gut Microbes</i> , 2022 , 14, 2068366	8.8	1
117	Characterisation of insomnia as an environmental risk factor for asthma via Mendelian randomization and gene environment interaction. <i>Scientific Reports</i> , 2021 , 11, 21813	4.9	2
116	A missense variant in SHARPIN mediates Alzheimer's disease-specific brain damages. <i>Translational Psychiatry</i> , 2021 , 11, 590	8.6	2
115	Appropriate number of observations for determining hand hygiene compliance among healthcare workers. <i>Antimicrobial Resistance and Infection Control</i> , 2021 , 10, 167	6.2	0
114	Unveiling Genetic Variants Underlying Vitamin D Deficiency in Multiple Korean Cohorts by a Genome-Wide Association Study. <i>Endocrinology and Metabolism</i> , 2021 ,	3.5	1
113	Identification of genetic loci affecting body mass index through interaction with multiple environmental factors using structured linear mixed model. <i>Scientific Reports</i> , 2021 , 11, 5001	4.9	1
112	Prenatal lead exposure and cord blood DNA methylation in the Korean Exposome Study. <i>Environmental Research</i> , 2021 , 195, 110767	7.9	6
111	Novel recessive locus for body mass index in childhood asthma. <i>Thorax</i> , 2021 , 76, 1227-1230	7.3	0
110	Microbiome profiling of uncinate tissue and nasal polyps in patients with chronic rhinosinusitis using swab and tissue biopsy. <i>PLoS ONE</i> , 2021 , 16, e0249688	3.7	3
109	Predicting allergic diseases in children using genome-wide association study (GWAS) data and family history. <i>World Allergy Organization Journal</i> , 2021 , 14, 100539	5.2	2
108	Fluoroquinolone and no risk of Achilles-tendinopathy in childhood pneumonia under eight years of age-a nationwide retrospective cohort. <i>Journal of Thoracic Disease</i> , 2021 , 13, 3399-3408	2.6	1
107	Nonalcoholic Fatty Liver Disease for the Incidence of Drug-Induced Liver Injury. <i>Clinical Gastroenterology and Hepatology</i> , 2021 ,	6.9	0

106	A high degree of knee flexion after TKA promotes the ability to perform high-flexion activities and patient satisfaction in Asian population. <i>BMC Musculoskeletal Disorders</i> , 2021 , 22, 565	2.8	0
105	Genome-wide association study of non-tuberculous mycobacterial pulmonary disease. <i>Thorax</i> , 2021 , 76, 169-177	7.3	1
104	Analysis of the Interaction between Polygenic Risk Score and Calorie Intake in Obesity in the Korean Population. <i>Lifestyle Genomics</i> , 2021 , 14, 20-29	2	2
103	An interaction of the 17q12-21 locus with mold exposure in childhood asthma. <i>Pediatric Allergy and Immunology</i> , 2021 , 32, 373-376	4.2	
102	A novel locus for exertional dyspnoea in childhood asthma. <i>European Respiratory Journal</i> , 2021 , 57,	13.6	3
101	Integrated genetic and epigenetic analyses uncover MSI2 association with allergic inflammation. <i>Journal of Allergy and Clinical Immunology</i> , 2021 , 147, 1453-1463	11.5	1
100	The nationwide retrospective cohort study by Health Insurance Review and Assessment Service proves that asthma management decreases the exacerbation risk of asthma. <i>Scientific Reports</i> , 2021 , 11, 1442	4.9	
99	Interactions between NCRILC3s and the Microbiome in the Airways Shape Asthma Severity. <i>Immune Network</i> , 2021 , 21, e25	6.1	1
98	Genome-Wide Association Study of Korean Asthmatics: A Comparison With UK Asthmatics. <i>Allergy, Asthma and Immunology Research</i> , 2021 , 13, 609-622	5.3	0
97	Selenomonas: A marker of asthma severity with the potential therapeutic effect. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2021 ,	9.3	0
96	DNA methylation changes associated with prenatal mercury exposure: A meta-analysis of prospective cohort studies from PACE consortium. <i>Environmental Research</i> , 2021 , 204, 112093	7.9	1
95	Bifidobacterium bifidum strains synergize with immune checkpoint inhibitors to reduce tumour burden in mice. <i>Nature Microbiology</i> , 2021 , 6, 277-288	26.6	29
94	Phylogenetic tree-based microbiome association test. <i>Bioinformatics</i> , 2020 , 36, 1000-1006	7.2	2
93	Unsupervised Cluster Analysis of Patients With Aortic Stenosis Reveals Distinct Population With Different Phenotypes and Outcomes. <i>Circulation: Cardiovascular Imaging</i> , 2020 , 13, e009707	3.9	8
92	Optimal high-density lipoprotein cholesterol level for decreasing benign prostatic hyperplasia in men not taking statin medication: A historical cohort study. <i>Prostate</i> , 2020 , 80, 570-576	4.2	2
91	Genome-wide interaction study of single-nucleotide polymorphisms and alcohol consumption on blood pressure: The Ansan and Ansong study of the Korean Genome and Epidemiology Study (KoGES). <i>Genetic Epidemiology</i> , 2020 , 44, 300-310	2.6	1
90	Methylation quantitative trait loci analysis in Korean exposome study. <i>Molecular and Cellular Toxicology</i> , 2020 , 16, 175-183	1.6	8
89	A Between Ethnicities Comparison of Chronic Obstructive Pulmonary Disease Genetic Risk. <i>Frontiers in Genetics</i> , 2020 , 11, 329	4.5	4

88	Limitations of rapid diagnostic tests in malaria surveys in areas with varied transmission intensity in Uganda 2017-2019: Implications for selection and use of HRP2 RDTs. <i>PLoS ONE</i> , 2020 , 15, e0244457	3.7	6
87	The prognoses and postoperative outcomes of patients with both colorectal cancer and liver cirrhosis based on a nationwide cohort in Korea. <i>Annals of Surgical Treatment and Research</i> , 2020 , 99, 82-89	2	2
86	The Influence of Family History on Stage and Survival of Gastric Cancer According to the TGFB1 C-509T Polymorphism in Korea. <i>Gut and Liver</i> , 2020 , 14, 79-88	4.8	7
85	Progressive effects of single-nucleotide polymorphisms on 16 phenotypic traits based on longitudinal data. <i>Genes and Genomics</i> , 2020 , 42, 393-403	2.1	0
84	Chronic obstructive pulmonary disease and related phenotypes: polygenic risk scores in population-based and case-control cohorts. <i>Lancet Respiratory Medicine</i> , 2020 , 8, 696-708	35.1	29
83	Effect of 6p21 region on lung function is modified by smoking: a genome-wide interaction study. <i>Scientific Reports</i> , 2020 , 10, 13075	4.9	1
82	Molecular surveillance reveals the presence of pfhrp2 and pfhrp3 gene deletions in Plasmodium falciparum parasite populations in Uganda, 2017-2019. <i>Malaria Journal</i> , 2020 , 19, 300	3.6	8
81	Causal Evaluation of Laboratory Markers in Type 2 Diabetes on Cancer and Vascular Diseases Using Various Mendelian Randomization Tools. <i>Frontiers in Genetics</i> , 2020 , 11, 597420	4.5	1
80	Family-based exome sequencing combined with linkage analyses identifies rare susceptibility variants of MUC4 for gastric cancer 2020 , 15, e0236197		
79	Family-based exome sequencing combined with linkage analyses identifies rare susceptibility variants of MUC4 for gastric cancer 2020 , 15, e0236197		
78	Family-based exome sequencing combined with linkage analyses identifies rare susceptibility variants of MUC4 for gastric cancer 2020 , 15, e0236197		
77	Family-based exome sequencing combined with linkage analyses identifies rare susceptibility variants of MUC4 for gastric cancer 2020 , 15, e0236197		
76	Effect of population stratification on SNP-by-environment interaction. <i>Genetic Epidemiology</i> , 2019 , 43, 1046-1055	2.6	2
75	Longitudinal decline in lung function: a community-based cohort study in Korea. <i>Scientific Reports</i> , 2019 , 9, 13614	4.9	13
74	Longitudinal analysis to better characterize Asthma-COPD overlap syndrome: Findings from an adult asthma cohort in Korea (COREA). <i>Clinical and Experimental Allergy</i> , 2019 , 49, 603-614	4.1	15
73	SNP genotype calling and quality control for multi-batch-based studies. <i>Genes and Genomics</i> , 2019 , 41, 927-939	2.1	5
72	A genome-wide association study implicates in lymphangioleiomyomatosis pathogenesis. <i>European Respiratory Journal</i> , 2019 , 53,	13.6	8
71	Comparison of INDEL Calling Tools with Simulation Data and Real Short-Read Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019 , 16, 1635-1644	3	3

70	Promoter Polymorphism-219T/G is an Effect Modifier of the Influence of β on Alzheimer's Disease Risk in a Multiracial Sample. <i>Journal of Clinical Medicine</i> , 2019 , 8,	5.1	20
69	The preventive effect of metformin on progression of benign prostate hyperplasia: A nationwide population-based cohort study in Korea. <i>PLoS ONE</i> , 2019 , 14, e0219394	3.7	6
68	BALLI: Bartlett-adjusted likelihood-based linear model approach for identifying differentially expressed genes with RNA-seq data. <i>BMC Genomics</i> , 2019 , 20, 540	4.5	1
67	Heritability estimation of dichotomous phenotypes using a liability threshold model on ascertained family-based samples. <i>Genetic Epidemiology</i> , 2019 , 43, 761-775	2.6	
66	Novel Trajectories for Identifying Asthma Phenotypes: A Longitudinal Study in Korean Asthma Cohort, COREA. <i>Journal of Allergy and Clinical Immunology: in Practice</i> , 2019 , 7, 1850-1857.e4	5.4	8
65	Maternal exposures to persistent organic pollutants are associated with DNA methylation of thyroid hormone-related genes in placenta differently by infant sex. <i>Environment International</i> , 2019 , 130, 104956	12.9	29
64	Estimating Nationwide Prevalence of Live Births with Down Syndrome and Their Medical Expenditures in Korea. <i>Journal of Korean Medical Science</i> , 2019 , 34, e207	4.7	3
63	Femoral joint line restoration is a major determinant of postoperative range of motion in revision total knee arthroplasty. <i>Knee Surgery, Sports Traumatology, Arthroscopy</i> , 2019 , 27, 2090-2095	5.5	15
62	Uncertainty estimation of exposure factors for consumer products based on various sample sizes. <i>Food and Chemical Toxicology</i> , 2019 , 134, 110874	4.7	0
61	Type-2 Diabetics Reduces Spatial Variation of Microbiome Based on Extracellular Vesicles from Gut Microbes across Human Body. <i>Scientific Reports</i> , 2019 , 9, 20136	4.9	9
60	The use of bisphosphonates after joint arthroplasty is associated with lower implant revision rate. <i>Knee Surgery, Sports Traumatology, Arthroscopy</i> , 2019 , 27, 2082-2089	5.5	11
59	Perturbations of gut microbiome genes in infants with atopic dermatitis according to feeding type. <i>Journal of Allergy and Clinical Immunology</i> , 2018 , 141, 1310-1319	11.5	73
58	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 379-384	11.5	21
57	ONETOOL for the analysis of family-based big data. <i>Bioinformatics</i> , 2018 , 34, 2851-2853	7.2	12
56	Genome-wide assessment of gene-by-smoking interactions in COPD. <i>Scientific Reports</i> , 2018 , 8, 9319	4.9	14
55	Prenatal exposure to persistent organic pollutants and methylation of LINE-1 and imprinted genes in placenta: A CHECK cohort study. <i>Environment International</i> , 2018 , 119, 398-406	12.9	21
54	WISARD: workbench for integrated superfast association studies for related datasets. <i>BMC Medical Genomics</i> , 2018 , 11, 39	3.7	7
53	Genetic Polymorphisms Associated with the Neutrophil/Lymphocyte Ratio and Their Clinical Implications for Metabolic Risk Factors. <i>Journal of Clinical Medicine</i> , 2018 , 7,	5.1	2

52	Genome-wide association analysis identifies multiple loci associated with kidney disease-related traits in Korean populations. <i>PLoS ONE</i> , 2018 , 13, e0194044	3.7	13
51	Evaluation of 16S rRNA Databases for Taxonomic Assignments Using Mock Community. <i>Genomics and Informatics</i> , 2018 , 16, e24	1.9	38
50	Multiple genotype-phenotype association study reveals intronic variant pair on SIDT2 associated with metabolic syndrome in a Korean population. <i>Human Genomics</i> , 2018 , 12, 48	6.8	6
49	Incidence and risk of chronic obstructive pulmonary disease in a Korean community-based cohort. <i>International Journal of COPD</i> , 2018 , 13, 509-517	3	10
48	Biphasic regulation of tumorigenesis by PTK7 expression level in esophageal squamous cell carcinoma. <i>Scientific Reports</i> , 2018 , 8, 8519	4.9	12
47	Rare variant association test with multiple phenotypes. <i>Genetic Epidemiology</i> , 2017 , 41, 198-209	2.6	14
46	Selecting cases and controls for DNA sequencing studies using family histories of disease. <i>Statistics in Medicine</i> , 2017 , 36, 2081-2099	2.3	1
45	Gene-based segregation method for identifying rare variants in family-based sequencing studies. <i>Genetic Epidemiology</i> , 2017 , 41, 309-319	2.6	11
44	Body mass index change in gastrointestinal cancer and chronic obstructive pulmonary disease is associated with Dedicator of Cytokines 1. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2017 , 8, 428-436	10.3	7
43	Single Marker Family-Based Association Analysis Not Conditional on Parental Information. <i>Methods in Molecular Biology</i> , 2017 , 1666, 409-439	1.4	
42	Network analysis for count data with excess zeros. <i>BMC Genetics</i> , 2017 , 18, 93	2.6	7
41	Determination of secondhand smoke leakage from the smoking room of an Internet caf�. <i>Journal of the Air and Waste Management Association</i> , 2017 , 67, 1061-1065	2.4	3
40	Improving Disease Prediction by Incorporating Family Disease History in Risk Prediction Models with Large-Scale Genetic Data. <i>Genetics</i> , 2017 , 207, 1147-1155	4	7
39	Considering common sources of exposure in association studies - Urinary benzophenone-3 and DEHP metabolites are associated with altered thyroid hormone balance in the NHANES 2007-2008. <i>Environment International</i> , 2017 , 107, 25-32	12.9	41
38	On the association analysis of CNV data: a fast and robust family-based association method. <i>BMC Bioinformatics</i> , 2017 , 18, 217	3.6	1
37	Seasonal patterns of dengue fever and associated climate factors in 4 provinces in Vietnam from 1994 to 2013. <i>BMC Infectious Diseases</i> , 2017 , 17, 218	4	35
36	Effect of Pregnancy on Quantitative Medication Use and Relation to Exacerbations in Asthma. <i>BioMed Research International</i> , 2017 , 2017, 8276190	3	11
35	Association between Metabotropic Glutamate Receptor 1 Polymorphism and Cardiovascular Disease in Korean Adults. <i>Journal of Lipid and Atherosclerosis</i> , 2017 , 6, 29	3	0

34	Comparing family-based rare variant association tests for dichotomous phenotypes. <i>BMC Proceedings</i> , 2016 , 10, 181-186	2.3	4
33	LPEseq: Local-Pooled-Error Test for RNA Sequencing Experiments with a Small Number of Replicates. <i>PLoS ONE</i> , 2016 , 11, e0159182	3.7	4
32	Validation of Prediction Models for Mismatch Repair Gene Mutations in Koreans. <i>Cancer Research and Treatment</i> , 2016 , 48, 668-75	5.2	4
31	Efficient Strategy to Identify Gene-Gene Interactions and Its Application to Type 2 Diabetes. <i>Genomics and Informatics</i> , 2016 , 14, 160-165	1.9	3
30	FARVATX: Family-Based Rare Variant Association Test for X-Linked Genes. <i>Genetic Epidemiology</i> , 2016 , 40, 475-85	2.6	3
29	Family-Based Rare Variant Association Analysis: A Fast and Efficient Method of Multivariate Phenotype Association Analysis. <i>Genetic Epidemiology</i> , 2016 , 40, 502-11	2.6	7
28	Conditional estimation of local pooled dispersion parameter in small-sample RNA-Seq data improves differential expression test. <i>Journal of Bioinformatics and Computational Biology</i> , 2016 , 14, 1644006	1	
27	Clostridia in the gut and onset of atopic dermatitis via eosinophilic inflammation. <i>Annals of Allergy, Asthma and Immunology</i> , 2016 , 117, 91-92.e1	3.2	29
26	Family-based association analysis: a fast and efficient method of multivariate association analysis with multiple variants. <i>BMC Bioinformatics</i> , 2015 , 16, 46	3.6	8
25	Adjusting heterogeneous ascertainment bias for genetic association analysis with extended families. <i>BMC Medical Genetics</i> , 2015 , 16, 62	2.1	7
24	Association between the APOB rs1469513 polymorphism and obesity is modified by dietary fat intake in Koreans. <i>Nutrition</i> , 2015 , 31, 653-8	4.8	13
23	Alcohol intake and cardiovascular risk factors: A Mendelian randomisation study. <i>Scientific Reports</i> , 2015 , 5, 18422	4.9	52
22	A Significant Increase in the Incidence of Central Precocious Puberty among Korean Girls from 2004 to 2010. <i>PLoS ONE</i> , 2015 , 10, e0141844	3.7	47
21	On the Estimation of Heritability with Family-Based and Population-Based Samples. <i>BioMed Research International</i> , 2015 , 2015, 671349	3	10
20	Evaluation of Penalized and Nonpenalized Methods for Disease Prediction with Large-Scale Genetic Data. <i>BioMed Research International</i> , 2015 , 2015, 605891	3	3
19	FARVAT: a family-based rare variant association test. <i>Bioinformatics</i> , 2014 , 30, 3197-205	7.2	20
18	On the analysis of a repeated measure design in genome-wide association analysis. <i>International Journal of Environmental Research and Public Health</i> , 2014 , 11, 12283-303	4.6	5
17	Relationship of vitamin D binding protein polymorphisms and lung function in Korean chronic obstructive pulmonary disease. <i>Yonsei Medical Journal</i> , 2014 , 55, 1318-25	3	17

16	Robust analysis with related samples under the presence of population substructure and its application to body mass index. <i>Genes and Genomics</i> , 2014 , 36, 643-654	2.1	
15	Efficient strategy for detecting gene-gene joint action and its application in schizophrenia. <i>Genetic Epidemiology</i> , 2014 , 38, 60-71	2.6	5
14	A general framework for robust and efficient association analysis in family-based designs: quantitative and dichotomous phenotypes. <i>Statistics in Medicine</i> , 2013 , 32, 4482-98	2.3	10
13	On rare-variant analysis in population-based designs: decomposing the likelihood to two informative components. <i>Human Heredity</i> , 2013 , 76, 76-85	1.1	
12	Fine-scale mapping of disease susceptibility locus with Bayesian partition model. <i>Genes and Genomics</i> , 2012 , 34, 401-407	2.1	
11	Introducing EzTaxon-e: a prokaryotic 16S rRNA gene sequence database with phylotypes that represent uncultured species. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012 , 62, 716-721	2.2	4480
10	On the meta-analysis of genome-wide association studies: a robust and efficient approach to combine population and family-based studies. <i>Human Heredity</i> , 2012 , 73, 35-46	1.1	5
9	Variants in FAM13A are associated with chronic obstructive pulmonary disease. <i>Nature Genetics</i> , 2010 , 42, 200-2	36.3	295
8	Single-marker and two-marker association tests for unphased case-control genotype data, with a power comparison. <i>Genetic Epidemiology</i> , 2010 , 34, 67-77	2.6	16
7	On the genome-wide analysis of copy number variants in family-based designs: methods for combining family-based and population-based information for testing dichotomous or quantitative traits, or completely ascertained samples. <i>Genetic Epidemiology</i> , 2010 , 34, 582-90	2.6	6
6	Phase uncertainty in case-control association studies. <i>Genetic Epidemiology</i> , 2009 , 33, 463-78	2.6	2
5	Maximizing the Power of Genome-Wide Association Studies: A Novel Class of Powerful Family-Based Association Tests. <i>Statistics in Biosciences</i> , 2009 , 1, 125-143	1.5	5
4	Choosing an optimal method to combine P-values. <i>Statistics in Medicine</i> , 2009 , 28, 1537-53	2.3	90
3	On the analysis of genome-wide association studies in family-based designs: a universal, robust analysis approach and an application to four genome-wide association studies. <i>PLoS Genetics</i> , 2009 , 5, e1000741	6	37
2	Fine-scale linkage disequilibrium mapping: a comparison of coalescent-based and haplotype-clustering-based methods. <i>BMC Proceedings</i> , 2007 , 1 Suppl 1, S133	2.3	2
1	Extension of the Haseman-Elston regression model to longitudinal data. <i>Human Heredity</i> , 2006 , 61, 111-9.1	2.1	6